

What Is Claimed Is:

1. A process for forming a catalogued nucleic acid library from an organism sample comprised of a plurality of organism forms, comprising the steps of:
 - (a) forming a derived organism sample from an initial organism sample, such that the proportional representations of the constituents in said derived organism sample are adjusted to advantage by performing in any order, and at least one time, at least one step selected from the group consisting of: (i) subjecting a working organism sample to a process of selection, and (ii) recovering a fraction of a working organism sample having at least one desired characteristic;
 - (b) isolating an initial nucleic acid sample from said derived organism sample;
 - (c) forming a derived nucleic acid library from said initial nucleic acid sample, such that the proportional representations of the constituents in said nucleic acid library are adjusted to advantage by performing in any order, and at least one time, at least one step selected from the group consisting of: (i) subjecting a working nucleic acid sample to a period of selection, (ii) recovering a fraction of a working nucleic acid sample having at least one desired characteristic, and (iii) assembling a working nucleic acid sample into a nucleic acid library;

whereby said process provides a means for forming a nucleic acid library wherein the proportional representations of the constituents in said nucleic acid library are advantageously adjusted to increase the yield potential of said library when said library is screened, particularly when a potentially desirable nucleic acid target is underrepresented the organism source sample, and , particularly also when a potentially desirable nucleic acid target is underrepresented the nucleic acid source sample.

2. The process of forming a catalogued nucleic acid library according to claim 1 wherein performing the step of (a) forming a derived organism sample from an initial organism sample is comprised of resolving the heterogeneity of said initial organism sample according to at least one organism marker, and of forming a derived organism sample that is normalized with respect to the resolved heterogeneity.
3. The process of forming a catalogued nucleic acid library according to claim 2 wherein at least one of said at least one organism marker is selected from the group consisting of 16S rRNA probes and 18S rRNA probes.
4. The process of forming a catalogued nucleic acid library according to claim 1 wherein performing the step of (a) forming a derived organism sample from an initial organism sample is comprised of resolving the heterogeneity of said initial organism sample according to at least one organism marker, and of forming a derived organism sample that is selectively enriched with respect to the resolved heterogeneity.
5. The process of forming a catalogued nucleic acid library according to claim 4 wherein at least one of said at least one organism marker is selected from the group consisting of 16S rRNA probes and 18S rRNA probes.
6. The process of forming a catalogued nucleic acid library according to claim 1 wherein performing the step of (a) forming a derived organism sample from an initial organism sample is comprised of resolving the heterogeneity of said initial organism sample according to at least two organism markers, and of forming a derived organism sample that is advantageously adjusted with respect to the heterogeneity resolved according to each of said at least two organism markers.

7. The process of forming a catalogued nucleic acid library according to claim 1 wherein performing the step of (c) forming a derived nucleic acid library from said initial nucleic acid sample is comprised of resolving the heterogeneity of said initial nucleic acid sample according to at least one nucleic acid marker, and of forming a derived nucleic acid library that is normalized with respect the resolved heterogeneity.
8. The process of forming a catalogued nucleic acid library according to claim 7 wherein at least one of said at least one nucleic acid marker consists of the G+C content.
9. The process of forming a catalogued nucleic acid library according to claim 1 wherein performing the step of (c) forming a derived nucleic acid library from said initial nucleic acid sample is comprised of resolving the heterogeneity of said initial nucleic acid sample according to at least one nucleic acid marker, and of forming a derived nucleic acid library that is selectively enriched with respect the resolved heterogeneity.
10. The process of forming a catalogued nucleic acid library according to claim 9 wherein at least one of said at least one nucleic acid marker consists of the G+C content.
11. The process of forming a catalogued nucleic acid library according to claim 1 wherein performing the step of (c) forming a derived nucleic acid library from said initial nucleic acid sample is comprised of resolving the heterogeneity of said initial nucleic acid sample according to at least two nucleic acid markers, and of forming a derived nucleic acid library that is advantageously adjusted with respect to the heterogeneity resolved according to each of said at least two nucleic acid markers.
12. The process of forming a catalogued nucleic acid library according to claim 1 wherein performing the step of (a) forming a derived organism sample from an initial organism sample is comprised of resolving the heterogeneity of said initial organism sample according to at least one organism marker, and of forming a derived organism sample

that is normalized with respect to the resolved heterogeneity of said initial organism sample, and also wherein performing the step of (c) forming a derived nucleic acid library from said initial nucleic acid sample is comprised of resolving the heterogeneity of said initial nucleic acid sample according to at least one nucleic acid marker, and of forming a derived nucleic acid library that is normalized with respect to the resolved heterogeneity of said initial nucleic acid sample.

13. The process of forming a catalogued nucleic acid library according to claim 12 wherein at least one of said at least one organism marker is selected from the group consisting of 16S rRNA probes and 18S rRNA probes.
14. The process of forming a catalogued nucleic acid library according to claim 12 wherein at least one of said at least one nucleic acid marker consists of the G+C content.
15. The process of forming a catalogued nucleic acid library according to claim 1 wherein performing the step of (a) forming a derived organism sample from an initial organism sample is comprised of resolving the heterogeneity of said initial organism sample according to at least one organism marker, and of forming a derived organism sample that is normalized with respect to the resolved heterogeneity of said initial organism sample, and also wherein performing the step of (c) forming a derived nucleic acid library from said initial nucleic acid sample is comprised of resolving the heterogeneity of said initial nucleic acid sample according to at least one nucleic acid marker, and of forming a derived nucleic acid library that is selectively enriched with respect to the resolved heterogeneity of said initial nucleic acid sample.
16. The process of forming a catalogued nucleic acid library according to claim 15 wherein at least one of said at least one organism marker is selected from the group consisting of 16S rRNA probes and 18S rRNA probes.

17. The process of forming a catalogued nucleic acid library according to claim 15 wherein at least one of said at least one nucleic acid marker consists of the G+C content.
18. The process of forming a catalogued nucleic acid library according to claim 1 wherein performing the step of (a) forming a derived organism sample from an initial organism sample is comprised of resolving the heterogeneity of said initial organism sample according to at least one organism marker, and of forming a derived organism sample that is normalized with respect to the resolved heterogeneity of said initial organism sample, and also wherein performing the step of (c) forming a derived nucleic acid library from said initial nucleic acid sample is comprised of resolving the heterogeneity of said initial nucleic acid sample according to at least two nucleic acid markers, and of forming a derived nucleic acid library that is advantageously adjusted with respect to the heterogeneity resolved according to each of said at least two nucleic acid markers.
19. The process of forming a catalogued nucleic acid library according to claim 18 wherein at least one of said at least one organism marker is selected from the group consisting of 16S rRNA probes and 18S rRNA probes.
20. The process of forming a catalogued nucleic acid library according to claim 1 wherein performing the step of (a) forming a derived organism sample from an initial organism sample is comprised of resolving the heterogeneity of said initial organism sample according to at least one organism marker, and of forming a derived organism sample that is selectively enriched with respect to the resolved heterogeneity of said initial organism sample, and also wherein performing the step of (c) forming a derived nucleic acid library from said initial nucleic acid sample is comprised of resolving the heterogeneity of said initial nucleic acid sample according to at least one nucleic acid

marker, and of forming a derived nucleic acid library that is normalized with respect to the resolved heterogeneity of said initial nucleic acid sample.

21. The process of forming a catalogued nucleic acid library according to claim 20 wherein at least one of said at least one organism marker is selected from the group consisting of 16S rRNA probes and 18S rRNA probes.
22. The process of forming a catalogued nucleic acid library according to claim 20 wherein at least one of said at least one nucleic acid marker consists of the G+C content.
23. The process of forming a catalogued nucleic acid library according to claim 1 wherein performing the step of (a) forming a derived organism sample from an initial organism sample is comprised of resolving the heterogeneity of said initial organism sample according to at least one organism marker, and of forming a derived organism sample that is selectively enriched with respect to the resolved heterogeneity of said initial organism sample, and also wherein performing the step of (c) forming a derived nucleic acid library from said initial nucleic acid sample is comprised of resolving the heterogeneity of said initial nucleic acid sample according to at least one nucleic acid marker, and of forming a derived nucleic acid library that is selectively enriched with respect to the resolved heterogeneity of said initial nucleic acid sample.
24. The process of forming a catalogued nucleic acid library according to claim 23 wherein at least one of said at least one organism marker is selected from the group consisting of 16S rRNA probes and 18S rRNA probes.
25. The process of forming a catalogued nucleic acid library according to claim 23 wherein at least one of said at least one nucleic acid marker consists of the G+C content.

26. The process of forming a catalogued nucleic acid library according to claim 1 wherein performing the step of (a) forming a derived organism sample from an initial organism sample is comprised of resolving the heterogeneity of said initial organism sample according to at least one organism marker, and of forming a derived organism sample that is selectively enriched with respect to the resolved heterogeneity of said initial organism sample, and also wherein performing the step of (c) forming a derived nucleic acid library from said initial nucleic acid sample is comprised of resolving the heterogeneity of said initial nucleic acid sample according to at least two nucleic acid markers, and of forming a derived nucleic acid library that is advantageously adjusted with respect to the heterogeneity resolved according to each of said at least two nucleic acid markers.
27. The process of forming a catalogued nucleic acid library according to claim 26 wherein at least one of said at least one organism marker is selected from the group consisting of 16S rRNA probes and 18S rRNA probes.
28. The process of forming a catalogued nucleic acid library according to claim 1 wherein performing the step of (a) forming a derived organism sample from an initial organism sample is comprised of resolving the heterogeneity of said initial organism sample according to at least two organism markers, and of forming a derived organism sample that is advantageously adjusted with respect to the heterogeneity resolved according to each of said at least two organism markers, and also wherein performing the step of (c) forming a derived nucleic acid library from said initial nucleic acid sample is comprised of resolving the heterogeneity of said initial nucleic acid sample according to at least one nucleic acid marker, and of forming a derived nucleic acid library that is normalized with respect the resolved heterogeneity of said initial nucleic acid sample.

29. The process of forming a catalogued nucleic acid library according to claim 28 wherein at least one of said at least one nucleic acid marker consists of the G+C content.
30. The process of forming a catalogued nucleic acid library according to claim 1 wherein performing the step of (a) forming a derived organism sample from an initial organism sample is comprised of resolving the heterogeneity of said initial organism sample according to at least two organism markers, and of forming a derived organism sample that is advantageously adjusted with respect to the heterogeneity resolved according to each of said at least two organism markers, and also wherein performing the step of (c) forming a derived nucleic acid library from said initial nucleic acid sample is comprised of resolving the heterogeneity of said initial nucleic acid sample according to at least one nucleic acid marker, and of forming a derived nucleic acid library that is selectively enriched with respect the resolved heterogeneity of said initial nucleic acid sample.
31. The process of forming a catalogued nucleic acid library according to claim 30 wherein at least one of said at least one nucleic acid marker consists of the G+C content.
32. The process of forming a catalogued nucleic acid library according to any of claims 1-31 wherein the step of (b) isolating a nucleic acid sample from said derived organism sample is comprised of isolating genomic DNA, and wherein the step of (c) forming a derived nucleic acid library from said initial nucleic acid sample is comprised of forming a genomic DNA library, such that a catalogued genomic DNA library is formed.
33. The process of forming a nucleic acid DNA library according to any of claims 1-31 wherein the step of (b) isolating a nucleic acid sample from said derived organism

sample is comprised of isolating genomic gene cluster DNA, and wherein the step of (c) forming a derived nucleic acid library from said initial nucleic acid sample is comprised of forming a genomic gene cluster DNA library, such that a catalogued genomic gene cluster DNA library is formed.

34. The process of forming a catalogued nucleic acid library according to any of claims 1-31 wherein the step of (b) isolating a nucleic acid sample from a derived organism sample is comprised of isolating RNA, and wherein the step of (c) forming a derived nucleic acid library from said initial nucleic acid sample is comprised of forming a cDNA library, such that a catalogued cDNA library is formed.
35. The process of forming a catalogued nucleic acid library according to claim 1 wherein performing the step of (a) forming a derived organism sample from an initial organism sample is comprised of forming a derived organism sample that consists of essentially only direct environmental organisms such that a catalogued nucleic acid library is formed from essentially only direct environmental organisms.
36. The process of forming a catalogued nucleic acid library according to claim 1 wherein performing the step of (a) forming a derived organism sample from an initial organism sample is comprised of forming a derived organism sample that consists of essentially only direct environmental organisms, and wherein the step of (b) isolating a nucleic acid sample from said derived organism sample is comprised of isolating genomic DNA, and also wherein the step of (c) forming a derived nucleic acid library from said initial nucleic acid sample is comprised of forming a genomic DNA library, such that a catalogued genomic DNA library is formed from essentially only direct environmental organisms.
37. The process of forming a catalogued nucleic acid library according to claim 1 wherein performing the step of (a) forming a derived organism sample from an initial organism

sample is comprised of forming a derived organism sample that consists of essentially only direct environmental organisms, and wherein the step of (b) isolating a nucleic acid sample from said derived organism sample is comprised of isolating genomic gene cluster DNA, and also wherein the step of (c) forming a derived nucleic acid library from said initial nucleic acid sample is comprised of forming a genomic gene cluster DNA library, such that a catalogued genomic gene cluster DNA library is formed from essentially only direct environmental organisms.

38. The process of forming a catalogued nucleic acid library according to claim 1 wherein performing the step of (a) forming a derived organism sample from an initial organism sample is comprised of forming a derived organism sample that consists of essentially only direct environmental organisms, and wherein the step of (b) isolating a nucleic acid sample from said derived organism sample is comprised of isolating RNA, and also wherein the step of (c) forming a derived nucleic acid library from said initial nucleic acid sample is comprised of forming a cDNA library, such that a catalogued cDNA library is formed from essentially only direct environmental organisms.

39. A catalogued nucleic acid library formed from an organism sample comprised of a plurality of organisms, formed by process comprising the steps of:

- (a) forming a derived organism sample from an initial organism sample, such that the proportional representations of the constituents in said derived organism sample are adjusted to advantage by performing in any order, and at least one time, at least one step selected from the group consisting of: (i) subjecting a working organism sample to a process of selection, and (ii) recovering a fraction of a working organism sample having at least one desired characteristic;
- (d) isolating an initial nucleic acid sample from said derived organism sample;

- (e) forming a derived nucleic acid library from said initial nucleic acid sample, such that the proportional representations of the constituents in said nucleic acid library are adjusted to advantage by performing in any order, and at least one time, at least one step selected from the group consisting of: (i) subjecting a working nucleic acid sample to a period of selection, (ii) recovering a fraction of a working nucleic acid sample having at least one desired characteristic, and (iii) assembling a working nucleic acid sample into a nucleic acid library;

whereby said nucleic acid library having advantageously adjusted proportional representations of the constituents and having an improved yield potential when said library is screened, is serviceable for identifying a potentially desirable nucleic acid target, particularly when said potentially desirable nucleic acid target is underrepresented in an organism source sample, and particularly also when said potentially desirable nucleic acid target is underrepresented in a nucleic acid source sample.

40. The catalogued nucleic acid library according to claim 39 wherein the step of (b) isolating a nucleic acid sample from said derived organism sample is comprised of isolating genomic DNA, and wherein the step of (c) forming a derived nucleic acid library from said initial nucleic acid sample is comprised of forming a genomic DNA library, such that a catalogued genomic DNA library is formed.
41. The catalogued nucleic acid library according to claim 39 wherein the step of (b) isolating a nucleic acid sample from said derived organism sample is comprised of isolating genomic gene cluster DNA, and wherein the step of (c) forming a derived nucleic acid library from said initial nucleic acid sample is comprised of forming a

such that a catalytic cycle is formed according to claim 1, wherein the catalyst is a derived organotin compound of (c) forming a complex comprised of formyl

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$\mathcal{H}^1(\mathbb{R}^n)$ is the space of functions of bounded variation. The space $\mathcal{H}^1(\mathbb{R}^n)$ is a Banach space with the norm $\|u\|_{\mathcal{H}^1(\mathbb{R}^n)} = \|u\|_{L^1(\mathbb{R}^n)} + \|\nabla u\|_{L^1(\mathbb{R}^n)}$. The space $\mathcal{H}^1(\mathbb{R}^n)$ is a subspace of $L^1(\mathbb{R}^n)$. The space $\mathcal{H}^1(\mathbb{R}^n)$ is a Banach space with the norm $\|u\|_{\mathcal{H}^1(\mathbb{R}^n)} = \|u\|_{L^1(\mathbb{R}^n)} + \|\nabla u\|_{L^1(\mathbb{R}^n)}$. The space $\mathcal{H}^1(\mathbb{R}^n)$ is a subspace of $L^1(\mathbb{R}^n)$.